

10/534744

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/534744
Source: PCT
Date Processed by STIC: 5/20/5

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PCT

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/534,744

DATE: 05/20/2005

TIME: 12:17:24

Input Set : A:\47968-A Sequence Listing.txt
 Output Set: N:\CRF4\05202005\J534744.raw

3 <110> APPLICANT: University of Saskatchewan Technologies Inc.
 5 <120> TITLE OF INVENTION: PLANT STRESS TOLERANCE GENES, AND USES THEREFOR
 7 <130> FILE REFERENCE: 47968-PT
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/534,744
 C--> 9 <141> CURRENT FILING DATE: 2005-05-12
 9 <150> PRIOR APPLICATION NUMBER: US 60/426,012
 10 <151> PRIOR FILING DATE: 2002-10-14
 12 <160> NUMBER OF SEQ ID NOS: 4
 14 <170> SOFTWARE: PatentIn version 3.1
 16 <210> SEQ ID NO: 1
 17 <211> LENGTH: 1420
 18 <212> TYPE: DNA
 19 <213> ORGANISM: Bromus
 21 <220> FEATURE:
 22 <221> NAME/KEY: misc_feature
 23 <222> LOCATION: (1212)..(1212)
 24 <223> OTHER INFORMATION: n = a, c, g, or t
 27 <220> FEATURE:
 28 <221> NAME/KEY: CDS
 29 <222> LOCATION: (77)..(1231)
 30 <223> OTHER INFORMATION:
 W--> 32 <400> 1
 33 gtcgcaatcc attcagagca cgcaaaggcac gcgagcagct gcgcattcta gattcttagct 60
 35 cgggacgatc agatca atg gcg gtc atg tcg cgg tcc agg agg ctg gcg gcg 112
 36 Met Ala Val Met Ser Arg Ser Arg Arg Leu Ala Ala
 37 1 5 10
 39 ccc gcg ctg ctg gtg cta gcg ctg gcg gcc gtg gcc gtc gtc gag 160
 40 Pro Ala Leu Leu Val Leu Ala Leu Ala Val Ala Val Ala Glu
 41 15 20 25
 43 acg acg ctg gac ggc gcg gag gtg gcg ccg ggc aag gag gag tcg tcg 208
 44 Thr Thr Leu Asp Gly Ala Glu Val Ala Pro Gly Lys Glu Glu Ser Ser
 45 30 35 40
 47 tgg gcg ggg tgg gcc aag gac aag gtc tcg gaa ggc ctc ggc ctg gac 256
 48 Trp Ala Gly Trp Ala Lys Asp Lys Val Ser Glu Gly Leu Gly Leu Asp
 49 45 50 55 60
 51 aag atc tcc gag ggg ctc ggg aag cac cac gcc gac gag gag gag 304
 52 Lys Ile Ser Glu Gly Leu Gly Leu Lys His His Ala Asp Glu Glu Glu
 53 65 70 75
 55 gcc gcg cgc aag gcc gga cac acc gtc aag tcc gcc cgc gag acc gcc 352
 56 Ala Ala Arg Lys Ala Gly His Thr Val Lys Ser Ala Arg Glu Thr Ala
 57 80 85 90
 59 cag cac gcc tcc gag acg ggg agg cag gcg agc ggc aag gtg ggg 400
 60 Gln His Ala Ala Ser Glu Thr Gly Arg Gln Ala Ser Gly Lys Val Gly

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61	95	100	105	
63	gac gcc aag gag gcc gcg gag cag gcg acc ggg gcg gcc aac aag			448
64	Asp Ala Lys Glu Ala Ala Glu Gln Ala Ala Thr Gly Ala Ala Asn Lys			
65	110	115	120	
67	gcg ggg cag gcc aaa gac aag gcg gcg gag acg gtg aag ggc acg gcc			496
68	Ala Gly Gln Ala Lys Asp Lys Ala Ala Glu Thr Val Lys Gly Thr Ala			
69	125	130	135	140
71	ggc gag gcg tcc aag aag gcg gag cag gcc aag cac aag acc aag gag			544
72	Gly Glu Ala Ser Lys Lys Ala Glu Gln Ala Lys His Lys Thr Lys Glu			
73	145	150	155	
75	gcc gcg gag gcg gcc aag acg ggc gcc gag acg cac gag cggtcg			592
76	Ala Ala Glu Ala Ala Lys Thr Gly Ala Glu Thr His Glu Arg Ser			
77	160	165	170	
79	aag cag ggc aag gcc aag gtg gag gag atg gcc agg gag tgg tac gag			640
80	Lys Gln Gly Lys Ala Lys Val Glu Glu Met Ala Arg Glu Trp Tyr Glu			
81	175	180	185	
83	aga gcc aag cac acg gcc ggg gag ggg tac gag acg ctg aag caa acc			688
84	Arg Ala Lys His Thr Ala Gly Glu Gly Tyr Glu Thr Leu Lys Gln Thr			
85	190	195	200	
87	aag gac gcg gct gcg gag aag gca gca gca gcc aag gac gcc gcc acg			736
88	Lys Asp Ala Ala Ala Glu Lys Ala Ala Ala Lys Asp Ala Ala Thr			
89	205	210	215	220
91	aac aag gcc ggt gcc acg cag acg gcc gcg gag aag gca gca gca			784
92	Asn Lys Ala Gly Ala Ala Thr Gln Thr Ala Ala Glu Lys Ala Ala Ala			
93	225	230	235	
95	gcc aag gac acc gcc ggc ggt aag gcc aag gct gcg aag gac gct gcg			832
96	Ala Lys Asp Thr Ala Ala Gly Lys Ala Lys Ala Lys Asp Ala Ala			
97	240	245	250	
99	tgg gag gag aca ggc tct gcc aag gac gcc aca tgg cag gcg cag gag			880
100	Trp Glu Glu Thr Gly Ser Ala Lys Asp Ala Thr Trp Gln Ala Gln Glu			
101	255	260	265	
103	aag ctg aag caa tac aac gac gcc gct tcg gag aag gcc gcg gca gcc			928
104	Lys Leu Lys Gln Tyr Asn Asp Ala Ala Ser Glu Lys Ala Ala Ala			
105	270	275	280	
107	aag gac gcc gac gct gag aag gcc gcg gca gcc aag gac gcg gcg tgg			976
108	Lys Asp Ala Asp Ala Glu Lys Ala Ala Ala Lys Asp Ala Ala Trp			
109	285	290	295	300
111	aag aac gcc gag gcg gcc aag gga acg gtc gga gag aag gca ggg gcg			1024
112	Lys Asn Ala Glu Ala Ala Lys Gly Thr Val Gly Glu Lys Ala Gly Ala			
113	305	310	315	
115	gcc aag gac gcc acg ttg gag aag acc gag tcc gcg aag gac gcc gct			1072
116	Ala Lys Asp Ala Thr Leu Glu Lys Thr Glu Ser Ala Lys Asp Ala Ala			
117	320	325	330	
119	tgg gag acg gcg gag gcg aag ggc aag gct aac gag ggg tac gag			1120
120	Trp Glu Thr Ala Glu Ala Ala Lys Gly Lys Ala Asn Glu Gly Tyr Glu			
121	335	340	345	
123	aag gtg aag gag aag gac gcg acc aag gaa aag ctc ggc gag gtg aag			1168
124	Lys Val Lys Glu Lys Asp Ala Thr Lys Glu Lys Leu Gly Glu Val Lys			
125	350	355	360	

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W--> 127	gac	aag	gtc	acc	ggc	gca	gca	tcc	gac	ggc	aag	gcg	aag	aag	cnc	cgc	1216
128	Asp	Lys	Val	Thr	Gly	Ala	Ala	Ser	Asp	Gly	Lys	Ala	Lys	Xaa	Arg		
129	365				370					375					380		
131	aat	ggc	gac	gag	ctg	tgaatgaaca	cgatccatcc	gcatttcttg	ccatagttcc							1271	
132	Asn	Gly	Asp	Glu	Leu												
133					385												
135	ttcttccatg	aatgtttca	gtgttcttcg	agctagttt	ttttatgttg	ttccttttgt										1331	
137	acaataacgt	gtccccatatg	tattgaacca	tgcacgatca	aacaagtttc	tttctataaaa										1391	
139	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa													1420	
142	<210>	SEQ ID NO:	2														
143	<211>	LENGTH:	385														
144	<212>	TYPE:	PRT														
145	<213>	ORGANISM:	Bromus														
147	<220>	FEATURE:															
148	<221>	NAME/KEY:	misc_feature														
149	<222>	LOCATION:	(379)..(379)														
150	<223>	OTHER INFORMATION:	The 'Xaa' at location 379 stands for His, Arg, Pro, or Leu.														
152	<400>	SEQUENCE:	2														
154	Met	Ala	Val	Met	Ser	Arg	Ser	Arg	Arg	Leu	Ala	Ala	Pro	Ala	Leu	Leu	
155	1			5						10					15		
158	Val	Leu	Leu	Ala	Leu	Ala	Ala	Val	Ala	Val	Ala	Glu	Thr	Thr	Leu	Asp	
159				20						25					30		
162	Gly	Ala	Glu	Val	Ala	Pro	Gly	Lys	Glu	Glu	Ser	Ser	Trp	Ala	Gly	Trp	
163				35						40					45		
166	Ala	Lys	Asp	Lys	Val	Ser	Glu	Gly	Leu	Gly	Leu	Asp	Lys	Ile	Ser	Glu	
167		50				55								60			
170	Gly	Leu	Gly	Leu	Lys	His	His	Ala	Asp	Glu	Glu	Glu	Ala	Ala	Arg	Lys	
171		65				70					75				80		
174	Ala	Gly	His	Thr	Val	Lys	Ser	Ala	Arg	Glu	Thr	Ala	Gln	His	Ala	Ala	
175				85						90				95			
178	Ser	Glu	Thr	Gly	Arg	Gln	Ala	Ser	Gly	Lys	Val	Gly	Asp	Ala	Lys	Glu	
179				100						105				110			
182	Ala	Ala	Glu	Gln	Ala	Ala	Thr	Gly	Ala	Ala	Asn	Lys	Ala	Gly	Gln	Ala	
183		115				120								125			
186	Lys	Asp	Lys	Ala	Ala	Glu	Thr	Val	Lys	Gly	Thr	Ala	Gly	Glu	Ala	Ser	
187		130				135								140			
190	Lys	Lys	Ala	Glu	Gln	Ala	Lys	His	Lys	Thr	Lys	Glu	Ala	Ala	Glu	Ala	
191		145				150					155				160		
194	Ala	Ala	Lys	Thr	Gly	Ala	Glu	Thr	His	Glu	Arg	Ser	Lys	Gln	Gly	Lys	
195				165						170				175			
198	Ala	Lys	Val	Glu	Glu	Met	Ala	Arg	Glu	Trp	Tyr	Glu	Arg	Ala	Lys	His	
199			180							185				190			
202	Thr	Ala	Gly	Glu	Gly	Tyr	Glu	Thr	Leu	Lys	Gln	Thr	Lys	Asp	Ala	Ala	
203		195				200								205			
206	Ala	Glu	Lys	Ala	Ala	Ala	Lys	Asp	Ala	Ala	Thr	Asn	Lys	Ala	Gly		
207		210				215								220			
210	Ala	Ala	Thr	Gln	Thr	Ala	Ala	Glu	Lys	Ala	Ala	Ala	Lys	Asp	Thr		
211		225				230								235		240	
214	Ala	Ala	Gly	Lys	Ala	Lys	Ala	Ala	Lys	Asp	Ala	Ala	Trp	Glu	Glu	Thr	

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215 245 250 255
218 Gly Ser Ala Lys Asp Ala Thr Trp Gln Ala Gln Glu Lys Leu Lys Gln
219 260 265 270
222 Tyr Asn Asp Ala Ala Ser Glu Lys Ala Ala Ala Ala Lys Asp Ala Asp
223 275 280 285
226 Ala Glu Lys Ala Ala Ala Ala Lys Asp Ala Ala Trp Lys Asn Ala Glu
227 290 295 300
230 Ala Ala Lys Gly Thr Val Gly Glu Lys Ala Gly Ala Ala Lys Asp Ala
231 305 310 315 320
234 Thr Leu Glu Lys Thr Glu Ser Ala Lys Asp Ala Ala Trp Glu Thr Ala
235 325 330 335
238 Glu Ala Ala Lys Gly Lys Ala Asn Glu Gly Tyr Glu Lys Val Lys Glu
239 340 345 350
242 Lys Asp Ala Thr Lys Glu Lys Leu Gly Glu Val Lys Asp Lys Val Thr
243 355 360 365
W--> 246 Gly Ala Ala Ser Asp Gly Lys Ala Lys Lys Xaa Arg Asn Gly Asp Glu
247 370 375 380
250 Leu
251 385
254 <210> SEQ ID NO: 3
255 <211> LENGTH: 15
256 <212> TYPE: PRT
257 <213> ORGANISM: Bromus
259 <400> SEQUENCE: 3
261 Glu Thr Thr Leu Asp Gly Ala Glu Val Ala Pro Gly Lys Glu Glu
262 1 5 10 15
265 <210> SEQ ID NO: 4
266 <211> LENGTH: 6
267 <212> TYPE: PRT
268 <213> ORGANISM: Bromus
270 <400> SEQUENCE: 4
272 Lys Ala Ala Ala Lys
273 1 5

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 05/20/2005
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 1212
Seq#:1; Xaa Pos. 379
Seq#:2; Xaa Pos. 379

VERIFICATION SUMMARY

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Input Set : A:\47968-A Sequence Listing.txt
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L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:32 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:30
L:127 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:1168
M:341 Repeated in SeqNo=1
L:246 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:368